
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=7; day=13; hr=15; min=15; sec=4; ms=281;]

Reviewer Comments:

<210> 13

<211> 649

<212> PRT

<213> bovine SILVEr

The above <213> response is invalid, per 1.823 of the Sequence Rules. The only valid responses are: the Genus species of the organism, "Artificial Sequence", or "Unknown". "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section; please give the source of the genetic material. Same error in Sequences 17-18.

<210> 16

<211> 1584

<212> DNA

<213> artificial sequence

<220>

<223> RPE1

The above <223> response is an insufficient explanation of "<213> Artificial Sequence": please give the source of the genetic material.

Validated By CRFValidator v 1.0.3

Application No: 10565646 Version No: 3.0

Input Set:

Output Set:

Started: 2009-06-26 10:29:31.434

Finished: 2009-06-26 10:29:39.825

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 391 ms

Total Warnings: 12

Total Errors: 24

No. of SeqIDs Defined: 18

Actual SeqID Count: 18

Err	or code	Error D	escription						
E	320	Wrong	Nucleic	Acid	Designator,	ga	in	SEQID	(1)
E	320	Wrong	Nucleic	Acid	Designator,	gt	in	SEQID	(1)
E	320	Wrong	Nucleic	Acid	Designator,	gg	in	SEQID	(1)
E	320	Wrong	Nucleic	Acid	Designator,	ac	in	SEQID	(1)
E	320	Wrong	Nucleic	Acid	Designator,	gc	in	SEQID	(1)
E	320	Wrong	Nucleic	Acid	Designator,	gg	in	SEQID	(1)
E	320	Wrong	Nucleic	Acid	Designator,	gg	in	SEQID	(1)
E	320	Wrong	Nucleic	Acid	Designator,	ag	in	SEQID	(1)
E	320	Wrong	Nucleic	Acid	Designator,	ga	in	SEQID	(3)
E	320	Wrong	Nucleic	Acid	Designator,	gt	in	SEQID	(3)
E	320	Wrong	Nucleic	Acid	Designator,	gg	in	SEQID	(3)
E	320	Wrong	Nucleic	Acid	Designator,	ac	in	SEQID	(3)
E	320	Wrong	Nucleic	Acid	Designator,	gc	in	SEQID	(3)
E	320	Wrong	Nucleic	Acid	Designator,	gg	in	SEQID	(3)
E	320	Wrong	Nucleic	Acid	Designator,	gg	in	SEQID	(3)
E	320	Wrong	Nucleic	Acid	Designator,	ag	in	SEQID	(3)
E	320	Wrong	Nucleic	Acid	Designator,	ga	in	SEQID	(5)
E	320	Wrong	Nucleic	Acid	Designator,	gt	in	SEQID	(5)
E	320	Wrong	Nucleic	Acid	Designator,	ac	in	SEQID	(5)
E	320	Wrong	Nucleic	Acid	Designator,	gc	in	SEQID	(5)

Input Set:

Output Set:

Started: 2009-06-26 10:29:31.434 **Finished:** 2009-06-26 10:29:39.825

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 391 ms

Total Warnings: 12
Total Errors: 24
No. of SeqIDs Defined: 18

Actual SeqID Count: 18

Erro	r code	Error Description
		This error has occured more than 20 times, will not be displayed
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (12)
W	402	Undefined organism found in <213> in SEQ ID (13)
W	213	Artificial or Unknown found in <213> in SEQ ID (14)
W	213	Artificial or Unknown found in <213> in SEQ ID (15)
W	213	Artificial or Unknown found in <213> in SEQ ID (16)
W	402	Undefined organism found in <213> in SEQ ID (17)
W	402	Undefined organism found in <213> in SEQ ID (18)

SEQUENCE LISTING

<110> OULMOUDEN, AHMAD JULIEN, RAYMOND LAFORET, MARIE-PIERRE LEVEZIEL, HUBERT <120> USE OF SILVER GENE FOR THE AUTHENTICATION OF THE RACIAL ORIGIN OF ANIMAL POPULATIONS, AND OF THE DERIVATIVE PRODUCTS THEREOF <130> 0508-1156 <140> 10565646 <141> 2006-03-24 <150> PCT/FR2004/001952 <151> 2004-07-22 <150> FR/09161 <151> 2003-07-25 <160> 18 <170> PatentIn version 3.1 <210> 1 <211> 8146 <212> DNA <213> Bos taurus <220> <221> CDS <222> (30)..(104) <223> First CDS region <220> <221> CDS <222> (2326)..(2435) <223> Second CDS region <220> <221> CDS <222> (2582)..(2727) <223> Third CDS region <220> <221> CDS <222> (3804)..(3937) <223> Fourth CDS region <220> <221> CDS

<222> (4315)..(4475) <223> Fifth CDS region

```
<220>
<221> CDS
<222> (4733)..(5412)
<223> Sixth CDS region
<220>
<221> CDS
<222> (6321)..(6436)
<223> Seventh CDS region
<220>
<221> CDS
<222> (6681)..(6765)
<223> Eighth CDS region
<220>
<221> CDS
<222> (6876)..(7080)
<223> Ninth CDS region
<220>
<221> CDS
<222> (7188)..(7275)
<223> Tenth CDS region
<220>
<221> CDS
<222> (7899)..(8036)
<223> Eleventh CDS region
<400> 1
ggtctttggt tgctggaagg aagaacagg atg gat ctg gtg ctg aga aaa tac
                                                                    53
                              Met Asp Leu Val Leu Arg Lys Tyr
                                              5
ctt ctc cat gtg gct ctg atg ggt gtt ctt ctg gct gta ggg acc aca
                                                                  101
Leu Leu His Val Ala Leu Met Gly Val Leu Leu Ala Val Gly Thr Thr
   10
                       15
                                          20
gaa g gtgagtgtgg gatgttggac atgaacaagt gtgaatttgg ggttgcacac
                                                                  155
Glu
25
ctgctctggt ttttctctcc ctaaaatgga agatatcagt agtgcttcag gtgtctccca
                                                                  215
cccatttgat ttagtgagga catgggcaac tgagctccct ccccacatga agatttgggt
                                                                  275
gcatgtgtgt tcaggcactt gggactgaac ctgaaaacaa ccccatctac ctggatgggt
                                                                  335
gagagaacag tatgtctccg tggccctaat tttgagatgc tctgaatagt gagctggaac
                                                                  395
atgggtgcca aggtagtaaa atgagtggaa actcatttag gctttgtctc aggcacttgg
                                                                  455
gatagggtat ttaggagata gagaaagata ggagatagga gaaaggagaa agaggatgtg
                                                                  515
                                                                  575
gtattggata gaagggtaat gaggcacctc atcccctctt tgggatgggc atgggtgaac
                                                                  635
acageceagg ettttgttet ggggetggaa gagacaggea gaagggtete agetgageat
                                                                   695
gatggtgaga gggtctggaa tgtcccgtgc tgctctgagg agggaggatt gggagtggag
                                                                  755
                                                                  815
aaagaatggg gcatcttatg attctcttgt tcttgtggtg aggtattcag tgggataatt
ctagatcctc ccccaagaga atcaaccagg tttctggtac atgttagaga tggagtgagg
                                                                  875
                                                                  935
atagtctgtg atgtgcagaa atatctacat tgtaccccag tgcccccttt ctctagatcc
                                                                   995
ctggtctcac agacttcttg gaacttctcc ttgatctgac ttccctcatt catggtgtca
```

tttcaagtct tattctttta ctatgttcgt tattgtattc tggaaatatc ctgttcatat	1055
gtgtccaccc aaggctctta atatgttgtg cttacttttt ggatccagat ttttaaaatc	1115
ataaqaaqac atttttatat aqttcatqaa attttqcatq qactqaqttt qataattttq	1175
tttagtqtqa attaacattq tqtttattta aqaaaaaaa atatttttt acaqaaacct	1235
actgaatttq tagggtttta aaataacatg atgtctggga tttgcttttg aatgcttcag	1295
ccaaaaaaca aacqaacaac aaaaataaaq qataqataaa qcaaatqtqa caaaatqctq	1355
atagttqttq qaccttqqqq agacacatqc aqaqccatca catcactttt tttcagacat	1415
ctttcttggt cagttataat cattttgttt gtccccactc ccaatttcta cttgcctcta	1475
	1535
gtccatcete etcactgett gccaaagtga teettetaaa acacaaatet gatcatatte	
aaaaagcttt tgaagggtaa gttttatggt atatgccata tatcagtaca acaaacaaaa	1595 1655
tcgtctgagg tgccgttgcc tacaggataa agtccaaact cctttgcctg gcactccaag	
cccccactct atcttcttgg cctcatctct catgatgtac atcagccaca ttgctagtgt	1715
ctgctcatgg ccttctgcct agaatgcttt atgccccagc caactattta ctgtcttctt	1775
cagtegacea gagtgeaatt tacetgttta aaatetatea ttttgttata cattgtgeat	1835
gtctattatg gctcatatta agcaatgcct tggattatag taatttatgt atatgtctat	1895
ttcatatact ttaacctgaa ccccttcaga accatttctt tttcatttct taagttcttt	1955
gcacctagcc cagtgcctgg tacgtcgtgg gtattcagta gattaaaatg cactttaagg	2015
aacttccctt gttgtccatc aagtggctaa ggctctgtgc tcccaatgca ggggaccagg	2075
gttcaatctc aggtcaggga actagatccc acaggtcaca actaagagtt tgcaagccac	2135
aactacctga cctcacatgc cacaactaat cgaagatccc tcgtgctgca actaagtcct	2195
agtgcagtta aatatatttt tttaatgcac tttgaatgtg agaatgaatg atgtgtcaca	2255
gacactgttg tcccctgaga agggagtgag taatgatttg agggccctca tagtatatct	2315
tcctttttag ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag	2363
Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Arg Gln	
30 35	
sts and att and man two and are not tot and man two and man	0.411
ctc aga att aaa gca tgg aac aga cag ctg tat cca gag tgg aca gaa	2411
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu	2411
	2411
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu	2411
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50	2411
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc	
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 age cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg	
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc	
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 age cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60	2456
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 age cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttec Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat	2456 2516
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 age cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60	2456
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccctt	2456 2516 2576
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg	2456 2516
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 age cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttec Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu	2456 2516 2576
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg	2456 2516 2576
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 age cag ggg cet gae tge tgg aga g gtaggaactt ggeaatttee Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtae ttaggaagat agggaaggaa aaggcataca gggaggagaa gecaaggage taattaatge agetgeeett tteag gt gge cae ata tee etg aag gte age aat gat ggg cet aca etg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75	2456 2516 2576 2625
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc	2456 2516 2576
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgcctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser	2456 2516 2576 2625
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc	2456 2516 2576 2625
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgcctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90	2456 2516 2576 2625
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgcctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser	2456 2516 2576 2625
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgcctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90	2456 2516 2576 2625
Leu Arg Tle Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 agc cag ggg cet gac tgc tgg aga g gtaggaactt ggcaattec Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccett ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90 caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac ac acc atc	2456 2516 2576 2625
Leu Arg Tle Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 agc cag ggg cet gac tgc tgg aga g gtaggaactt ggcaattec Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccett ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90 caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac aac acc atc Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile	2456 2516 2576 2625
Leu Arg Tle Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 agc cag ggg cet gac tgc tgg aga g gtaggaactt ggcaattec Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccett ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90 caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac aac acc atc Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile	2456 2516 2576 2625
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cet gac tgc tgg aga g gtaggaactt ggcaatttee Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgeeett tteag gt gge cac ata tee etg aag gte age aat gat ggg cet aca etg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gea aat get tee tte tet att gee ttg cac ttt cet aaa age Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90 caa aag gtg etg cea gat ggg cag gte ate tgg gee aac aac ace ate Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile 95 100 105	2456 2516 2576 2625 2673
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgcctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90 caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac aac acc atc Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile 95 100 105	2456 2516 2576 2625 2673
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgcctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90 caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac ac acc atc Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile 95 100 105 atc aat g gtgagtacct ctccgcctcc ttcccaaggt ccagaatccc tggtatcccc Ile Asn	2456 2516 2576 2625 2673
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgcctt ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90 caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac ac acc atc Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile 95 100 105 atc aat g gtgagtacct ctccgcctcc ttcccaaggt ccagaatccc tggtatcccc Ile Asn	2456 2516 2576 2625 2673
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu 40 45 50 agc cag ggg cet gac tgc tgg aga g gtaggaactt ggcaatttec Ser Gln Gly Pro Asp Cys Trp Arg 55 60 agggaggata tggtggaaat gggtggggag gggaacgggg ttgaatgtac ttaggaagat agggaaggaa aaggcataca gggaggagaa gccaaggagc taattaatgc agctgccett ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu 65 70 75 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser 80 85 90 caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac aac acc atc Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile 95 100 105 atc aat g gtgagtacct ctccgcctcc ttcccaaggt ccagaatccc tggtatcccc Ile Asn 110	2456 2516 2576 2625 2673 2721

tagttcccca aatggggcac agaagaccca gtggacatag aagttggata gacttggatt 2958

taaactggtt accagtatgt gaccctggac aagtcactga attgttttgt tcttccattc	3018
ccttatctat agaatgggga tgataacact ttaaaaggtt cttgtaagga ttaaaatgtg	3078
ataatatata aagattttag cataatgeet geeetgtget gtgettagta eettagttta	3138
gacgetttge aaccecatgg actgtagece accaggetee tetgtecatg tggattetge	3198
aggcaagaat actggagtgg gtcaccatgc actcctccag gggatcttcc caactcaggg	3258
atcgaaccca ggtcctagcc tacagtatta attgatgctg ttatttttac ttttatccca	3318
ctagctagag cacatcatcc tagacatttt gatacatggc ctaccaattt gtgtccagtg	3378
taagaatata catgtgtgtg ctcagtggct cagtcgtgtc tgactctttg caaccccatg	3438
gactgtagcc cgcgaaagct cctctgccca tgggattgcc cagccaagaa tactggagca	3498
ggttgccatt tcttcctcca ggggatcttt caacacaggg attgaatcct tgtctcctgt	3558
gtttcctgca ttggcaggtg tattctttac cactgagcca cctgggaaac cccttaagta	3618
tatacacata aatcttttat agtttccatt ctcccttcta ccactccaaa taggttatac	3678
caaggagaat gtattttggt agctaggcag tattcctgga gcccctctct gggagtcatg	3738
ttaaaggttt tggtgtacag tgaggaatgc cagggattga gggagacttg ctgtcttctt	3798
ttcag gg agc cag gtg tgg gga gga cag ctg gta tat ccc caa gaa cct Gly Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro 115 120 125	3847
gat gat acc tgc atc ttc ccc gat ggg gag ccc tgc cct tct ggc cct Asp Asp Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro 130 135 140	3895
cta tct cag aaa aga tgc ttt gtt tat gtc tgg aag acc tgg g Leu Ser Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp 145 150 155	3938
gtaagagttt cccttctctg gcctgtcatt cacacttaaa ttcacttctt cctacctgat	3998
cccctttctt ttggtctcat ccttaaattc tgtgagtttc cctaatcttc acttccccca	4058
tgactccttc ctcttccaca gcacctagtc aactctatta tacttctttc tgggagccct	4118
gctccaatta tagtcccatc ccatggaccc tctcataagg acttttttcc tgcccaacat	4178
atgcaagctt aaactctctg aaataaccat ccttgataca tctcctgacc ttccttctct	4238
ggttccatct ctaaccctgc cccagtctcc tttgaccagt aacccccttc cctactcttc	4298
tttccaaaaa cctcag ac caa tac tgg caa gtt ctg ggg ggc cca gtg tct Asp Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser 160 165	4349
gga ctg agc atc ggg aca gac aag gca atg ctg ggc aca tat aac atg Gly Leu Ser Ile Gly Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met 170 175 180	4397
gaa gtg act gtc tac cac cgc cgg ggg tcc cag agc tat gtg ccc ctc Glu Val Thr Val Tyr His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu 185 190 195 200	4445
gct cac tcc agt tca gcc ttc acc att act g gtaaggactg aggagggac Ala His Ser Ser Ser Ala Phe Thr Ile Thr 205 210	4496
aaqqccaqtt qcaqqqcaqq aqaaqqtqqq qaqqctqqqc tqqacaqqaa aqqqqaaaqa	4556
ggaaatggtg tgtaacctta caggggcaga accaggaaga tgtgggcaga gggatgtggg	4616
gcttggagcc cgtgaagggc caggcagctt gggttggttg aaaaatatgg ctgtgaaaga	4676
agaagetgae agaaagaaga aettatggtt eteaetttet etgaeteeaa teecag ae	4734

Asp

_						_			cag Gln	_	_	-	_	_		4782	
		_	-		-	-	_	-	cct Pro	_			-		_	4830	
		-		_			_	_	ggg	_	_					4878	
	-			-	-				ctg Leu				-		-	4926	
-									cca Pro 285	-		-	_			4974	
_	-	-	-						tgt Cys					-		5022	
			_						gca Ala		_					5070	
-							-	_	atg Met						-	5118	
			-		-				aca Thr	-						5166	
		_	-						cag Gln 365		_				=	5214	
	_						_		act Thr	_		_				5262	
		_							tct Ser				_		_	5310	
					_				aca Thr	_						5358	
								_	tca Ser		_			_		5406	

420 425 430 435

act gca g gtaagggggc caccatgaat gagttcatag aggtggggca tttgtcacag Thr Ala	5463
ctctgaagac ctgaaagaat tgctcaggac ccagatgtta ctcaatcctt agcttagcag tggagtcccc tcagaatctt cactggtttt aaaaccccct aagtcctct taatggcaca gaatagatcc agagttcagg aaaccagggt cttctcctag gccaggggta gagagcttat tctctctcc tgaagagaag ttcaggaagc agtgtgtgat catttggtgg tggtgccag tcatgctga ctctttgtga cctcatggac tatggcccac caggctcctc tgtccataga attctccagg caagaacact ggagtgggtg gccatttcct tctccagggg attttccctg cccagggatt aaacccgaat tggcaggtgg attcttacc cgagccacct agaaagtccc atgtgatcat tagataatac ttatacctca ttttctgatt aagtgtaaac acagaaatct ttctgacacc acttcccacc cctggattcc catcccaaag taggttacc tggaattgtg gtaggaatac taaaaaaggga gaagtgagat agtgacacta tgacttaaca catgtcaaat gtctgaccca ggacctggca cagtgtaggg tgtgataaac atttgggatg tctaaaattc tgactcaac cctgtgactc tggggcagtc atttctttg ggcctttct tatcttaaaa aatgagagt tccagctctt gtctgattct aagcctggat ccagtagct tgacttacc tggaaaaatg cttgtagaaaaatg cttgttgggc ctgttttcag gttagtcatt tgctttttga ctttgcctct tggaaaaaatg cttgttggaaaaaatg cttgttgggc ctgttttcag gttagtcatt tgctttttga ctttgcctct	5523 5583 5643 5703 5763 5823 5883 5943 6003 6063 6123 6183 6243 6303
ttaatcetet eetecag ge tee etg agt eee etg eeg gat gae aet gee Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala 440 445	6352
acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr 450 455 460	6400
cgc tat ggc tcc ttt tcc ctc acc ctg gac att gtc c gtgagtcttg Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val 465 470 475	6447
cctacattgt ccgtaagctg gtggagggag gcgtgtgctg cttagggttg cccagtggaa gcacaccttg gaaggaatta ctcacctgga caaggagaat acccagatcc caggggtttc atatgaaggc agaatgggat tagggaggca gcccgaggac cttcctggcc atgggccttg	6507 6567 6627
ggggaggata agtagaggag teteagaett aaaaaaatet tgeaaetttg eag ag Gln	6682
ggt att gag agt gct gag atc cta cag gct gtg tca tcc agt gaa gga Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly 480 485 490	6730
gat gca ttt gag ctg act gtg tct tgc caa ggc gg gtgagtgtcc Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly 495 500 505	6775
cacggttgcc ctgagaactc ctggggtgac tgctgtcctg ttctctggtg tctagtgtcc	6835
cttcccagat tccctgacgt aagctgacat ctctcccag g cta ccc aag gaa gcc Leu Pro Lys Glu Ala 510	6890
tgc atg gac atc tca tcg cca ggg tgt cag ctg cct gcc cag cgg ctg Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu 515 520 525	6938

_	_		gtg Val 530			-		-	_	_	_	-	_		_	6986
-	_	_	ggt Gly						-						-	7034
			agc Ser												g	7080
gtag	ggtag	gtt (ggaca	aagaq	gg ta	aggat	gaaq	g aca	acgg	ggag	atg	gtaga	agg t	taco	ctacta	7140
			ggaca										gg		gaa	7140 7195
gago	gaag	cag a		:gaat	ig ca	agcc	gtato	c tgọ	ggatt	cca	ccca	atag	gg Gly	caa Gln 575	gaa Glu	
gago gca	gaago	cag a	acact	cag	gct	agccq cct	gtato	c tgg	ggatt gtg	ggc	ccca	atag ttg	gg Gly ctg	caa Gln 575 gtg	gaa Glu cta	7195
gago gca	gaago	cag a	acact agg	cag	gct	agccq cct	gtato	c tgg	ggatt gtg	ggc	ccca	atag ttg	gg Gly ctg	caa Gln 575 gtg	gaa Glu cta	7195